

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 27.1047 Seconds

(Without alignments)  
843.812 Million cell updates/sec

Title: US-09-622-613B-26

Perfect score: 606  
Sequence: 1 NSMATEFOOKHINTPILCN.....ICVKCENQYVPHAGICRCP 111

Scoring table: BUCSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	586.5	96.8	133	09PWR7	09PWR7 rana catesb
2	585.5	91.7	133	098SM0	098SM0 rana catesb
3	482.5	79.6	133	098SM2	098SM2 rana catesb
4	473.5	78.1	133	098SL9	098SL9 rana catesb
5	466.5	77.0	133	098SL8	098SL8 rana catesb
6	443.5	73.2	133	098SM1	098SM1 rana catesb
7	371	61.2	133	09PDR7	09PDR7 rana catesb
8	276.5	45.6	133	09PDR8	09PDR8 rana catesb
9	272.5	45.0	127	0918V8	0918V8 rana pipien
10	241	39.8	129	09DFY6	09DFY6 rana catesb
11	224.5	37.0	128	09DFY8	09DFY8 rana catesb
12	221.5	36.5	128	09DFY7	09DFY7 rana catesb
13	212.5	35.1	128	09DFY5	09DFY5 rana catesb
14	158	26.1	169	09W738	09W738 xenopus lae
15	131	21.6	170	09BEC1	09BEC1 tragulus ja
16	126	20.8	150	08VD94	08VD94 berylmys bo

17	125.5	20.7	163	6	09BDC2	09BDC2 antilocapra
18	124.5	20.5	116	6	09VVC0	09VVC0 sus scrofa
19	124	20.5	150	11	08VDB8	08VDB8 rattus norv
20	122.5	20.2	144	6	09BH14	09BH14 antilocapra
21	120	19.8	150	11	08VDB2	08VDB2 rattus exul
22	116.5	19.2	152	11	08VDB9	08VDB9 rattus norv
23	115.5	19.1	119	6	09TV33	09TV33 bos taurus
24	114.5	18.9	124	6	095NE6	095NE6 bubalus bub
25	112.5	18.6	149	11	08VDP5	08VDP5 berylmys bo
26	112	18.5	134	6	09BDB9	09BDB9 tragulus ja
27	111.5	18.4	152	11	08VDB4	08VDB4 rattus tiom
28	111.5	18.4	156	6	08SQ05	08SQ05 lagotrichix 1
29	110.5	18.2	119	6	09TV30	09TV30 saquinus oe
30	110.5	18.2	119	6	09TV28	09TV28 cullemur ful
31	110.5	18.2	124	6	09TSF2	09TSF2 bos taurus
32	109.5	18.1	142	6	09BEC3	09BEC3 tragulus ja
33	109.5	18.1	156	6	08SQ06	08SQ06 ateles geot
34	109	18.0	124	6	09BEC2	09BEC2 tragulus ja
35	108.5	17.9	156	6	08SQ08	08SQ08 salimiri sci
36	108.5	17.9	156	6	08SQ07	08SQ07 saquinus oe
37	107.5	17.7	152	11	08VDP0	08VDP0 rattus fusc
38	106.5	17.6	116	6	097933	097933 phocoenoid
39	106.5	17.6	149	11	08VDP3	08VDP3 rattus exul
40	105.5	17.4	116	6	097934	097934 pseudorca c
41	105.5	17.4	119	6	09TS06	09TS06 cercopthec
42	105.5	17.4	157	11	09JRK4	09JRK4 meriones un
43	105	17.3	158	6	08SPY2	08SPY2 callithrix
44	104.5	17.2	119	6	09TV32	09TV32 gorilla gor
45	104.5	17.2	124	6	09XS40	09XS40 camelus bac

# ALIGNMENTS

## RESULT 1

ID	Q9PWR7	PRELIMINARY:	PRT:	133 AA.
AC	Q9PWR7:			
DT	01-MAY-2000 (TREMBLREL. 13, Created)			
DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLREL. 19, Last annotation update)			
DE	Ribonuclease precursor.			
GN	RCR.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RX	MEDLINE=98165825; PubMed=9497370;			
RA	Huang H.C., Wang S.C., Liew Y.J., Lu S.C., Liao Y.D.;			
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.			
RT	Tissue distribution, cloning, purification, cytotoxicity, and active			
RT	residues for RNase activity."			
RL	J Biol Chem. 273:6395-6401(1998).			
DR	EMBL, AF039104; AAD10702.1; -			
DR	HSSP; P11916; 18C4.			
DR	InterPro; IPR001427; RNaseA.			
DR	Pfam; PF00074; rnaaseA.1.			
DR	ProDom; PD000535; RNaseA.1.			
DR	SMART; SM00092; RNase_PC.1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN			
FT	REGION			
SO	SEQUENCE			
Query Match	96.88;	Score 586.5;	DB 13;	Length 133;
Best Local Similarity	99.18;	Pred. No. 3.4e-60;		
Matches 109;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
Oy	3	NSMATEFOOKHINTPILCN	NTIMDNINIVVGQCKRVNFTIISATVTKAICTGVANNVL	61

Db 24 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 83  
 QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 111  
 Db 84 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 133

## RESULT 2

Q98SMO PRELIMINARY: PRT: 133 AA.  
 ID Q98SMO  
 AC 098SMO  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc208 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roseberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351209; AAK30255.1; -  
 DR HSSP: P1916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 133 AA: 14528 MW: 87FCF12C3499E02 CRC64;  
 Query Match .91.7%; Score 555.5; DB 13; Length 133;  
 Best Local Similarity 94.5%; Pred. No. 1.3e-56;  
 Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 3 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 61  
 Db 24 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 83  
 QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 111  
 Db 84 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 133

## RESULT 3

Q98SMO PRELIMINARY: PRT: 132 AA.  
 ID Q98SMO  
 AC 098SMO  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roseberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1; -  
 DR HSSP: P1916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;  
 Query Match 78.1%; Score 473.5; DB 13; Length 133;  
 Best Local Similarity 78.2%; Pred. No. 4.1e-47;  
 Matches 86; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

RP TISSUE=LIVER;  
 RC

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF351207; AAK30253.1; -  
 DR EMBL: AF359578; AAL87036.1; -  
 DR HSSP: P1916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 132 AA: 14412 MW: 131A745187978687 CRC64;

Query Match 79.6%; Score 482.5; DB 13; Length 132;  
 Best Local Similarity 84.3%; Pred. No. 3.7e-48;  
 Matches 91; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

OY 4 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 62  
 Db 25 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 84  
 QY 63 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 110  
 Db 85 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 132

## RESULT 4

Q98SL9 PRELIMINARY: PRT: 133 AA.  
 ID Q98SL9  
 AC 098SL9  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE RNase A-type ribonuclease rc212 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Roseberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana.";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL: AF351210; AAK30256.1; -  
 DR HSSP: P1916; IBC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 133 AA: 14615 MW: C8785B236B2654E CRC64;  
 Query Match 78.1%; Score 473.5; DB 13; Length 133;  
 Best Local Similarity 78.2%; Pred. No. 4.1e-47;  
 Matches 86; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

OY 3 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 61  
 Db 24 NMATFOCKHIINTPIT-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 83

QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 111  
 Db 84 STTRFQNTCTRTSITPRPCPYSSRTETNYICVCENQYPVHFGIGRC 133

## RESULT 5

Q98SL8

ID	098SL8	PRELIMINARY;	PRT;	133 AA.
AD	098SL8			
AC	098SL8			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RNase A-type ribonuclease rc218 precursor.			
OS	Rana catesbeiana (Bull) frog.			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21539506; PubMed=11683320;			
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;			
RT	"Rapid diversification of RNase A superfamily ribonuclease from the			
RT	bullfrog, Rana catesbeiana.";			
RL	J. Mol. Evol. 53:31-38(2001).			
DR	EMBL: AF31211; AAK30257.1; -			
DR	HSSP; P11916; 1BC4.			
DR	InterPro; IPR001427; RNaseA.			
DR	Pfam; PF00074; rna5a; 1.			
DR	ProDom; PD000515; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1;			
KW	Signal.			
FT	SIGNAL	1	22	POTENTIAL.
SO	SEQUENCE	133 AA;	14590 MM;	8BA0B9A94FA5B943 CRC64;
Query Match		77.0%;	Score 466.5;	DB 13; Length 133;
Best Local Similarity		76.4%;	Pred. No. 2.6e-46;	
Matches	84;	Conservative 13;	Mismatches 12;	Indels 1; Gaps 1
Oy	3 MMATEGCKKHINTPLI-CNTIDNNIYIVGGCKRVNFISSATTAICTYATINMVL 61			
Db	24 MMATEGEOHINTSSINSINMNSLYIVGGCKVNFIISSATTAIVGICGVADKKVL 83			
Oy	62 STTRFQNLTCRTSTTRPRPCYSSTETENIYICVKNQPVHFAIGRCR 111			
Db	84 SSTRFQDICTRIFTRPRPCYSSTETENIYICVKNQPVHFAIGRCR 133			

[illegible]





RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF159166; ADD1901.1; -

DR HSSP: P00656; 1LSO.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_PC; 1.

DR PROSITE: PS00127; RNase\_PANCREATIC; UNKNOWN.1.

SO SEQUENCE 169 AA; 18891 MW; D969F3EA3B3CE1B8 CRC64;

Query Match 26.18; Score 158; DB 13; Length 169;

Best Local Similarity 38.78; Pred. No. 1.8e-10;

Matches 43; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

3 NMATFOCKHII--NTPLICN-TIMDNIYIGGCKRNVNFI-SSATVKAICTGVINM 58

29 NINAFMEKHIVKEAEETNCNOTIKDRNIRF-KNCKFRNFTIHDTNGKKVEMCAGIVKS 87

59 N-VLSTTRFOLNCTRTSTPRP--CPYSSRTETNYICVGCENQYPVHFAG 106

88 TFAISKELLPLTDCLLMGRTARPNCAYNQTRTGTGINTCENNYPVHFAG 138

RESULT 15

Q9BEC1 PRELIMINARY; PRT; 170 AA.

AC Q9BEC1

DT 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Brain-type ribonuclease ribonuclease precursor (Fragment).

GN RNase B.

OS Tragus javanicus (Lesser Malay chevrotain).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;

OC Tragulidae; Tragulus.

OC NCBI\_TaxID=9849;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-21347458; Pubmed-11453981;

RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,

Warmeris H.W., Beintema J.O.,

RT "Secretory ribonucleases in the primitive ruminant chevrotain

(Tragus javanicus)."

RL Eur. J. Biochem. 268:3890-3897(2001).

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR EMBL: AJ271299; CAC24723.1; -

DR HSSP: P00656; 1LSO.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_PC; 1.

DR PROSITE: PS00127; RNase\_PANCREATIC; 1.

KW Endonuclease; Hydrolase; Nuclease; Signal.

FT NON\_TER 1

FT SIGNAL <1 19

FT CHAIN 20 170

SO SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;

Query Match 21.68; Score 131; DB 6; Length 170;

Best Local Similarity 33.14; Pred. No. 2.4e-07;

Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

5 ATFOQKHII-----INPIICNTIMDNIYIGGCKRNVNFISSATVKAICT----- 53

25 AKFRROHLDGNSINSN-YCNLMKRR-KMTHGRCKPVNFTIHESLEADVKAICSEKNIT 82

54 ---GVIMANVLTSTRFOLNCTRTSTPRP--CPYSSRTETNYICVGCEN--QYPVHFAGI 107

83 CKNGQPMCHOSNST-MNITDCROTGGSKYPCAYKTSQKOKYIIVACEGTPVPVHFDGS 141

OY 108 GRCP 111

DB 142 AVLP 145

Search completed: June 25, 2003, 14:55:27  
Job time : 28.188 secs